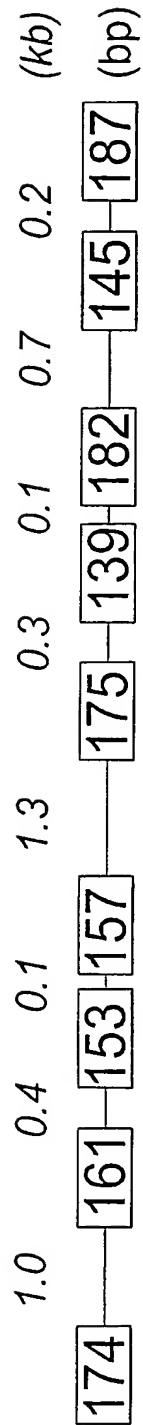


Fig 1A 1/15



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Fig 1B

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atg gcc ctg ctg ctc ttg ctg ttc ctg ggc ctc ctg ggg ctc tgg ggg	48
Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu Leu Gly Leu Trp Gly	
1 5 10 15	
ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca gct gcc cgg tgg ccc	96
Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro	
20 25 30	
ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac ctg cac ttg ctg cgt	144
Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg	
35 40 45	
ctg tgc caa cag gac cgg tcc ctg atg gag ctc tca gaa cgc tac ggg	192
Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly	
50 55 60	
ccg gtg ttc acc gtg cac ctg ggg cgc cag aag acg gtg gtg ctg acg	240
Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr	
65 70 75 80	
ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg	288
Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu	
85 90 95	
gcc gac cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga	336
Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly	
100 105 110	
ggc atc ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc	384
Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Arg Gln Phe	
115 120 125	
acg gtg cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct	432
Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala	
130 135 140	
gac aag att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc	480
Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly	
145 150 155 160	
tac aga ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc	528
Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser	
165 170 175	
aat atc acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac	576
Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp	
180 185 190	
ccc gtg ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc	624
Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu	
195 200 205	

## Fig 1B (cont.)

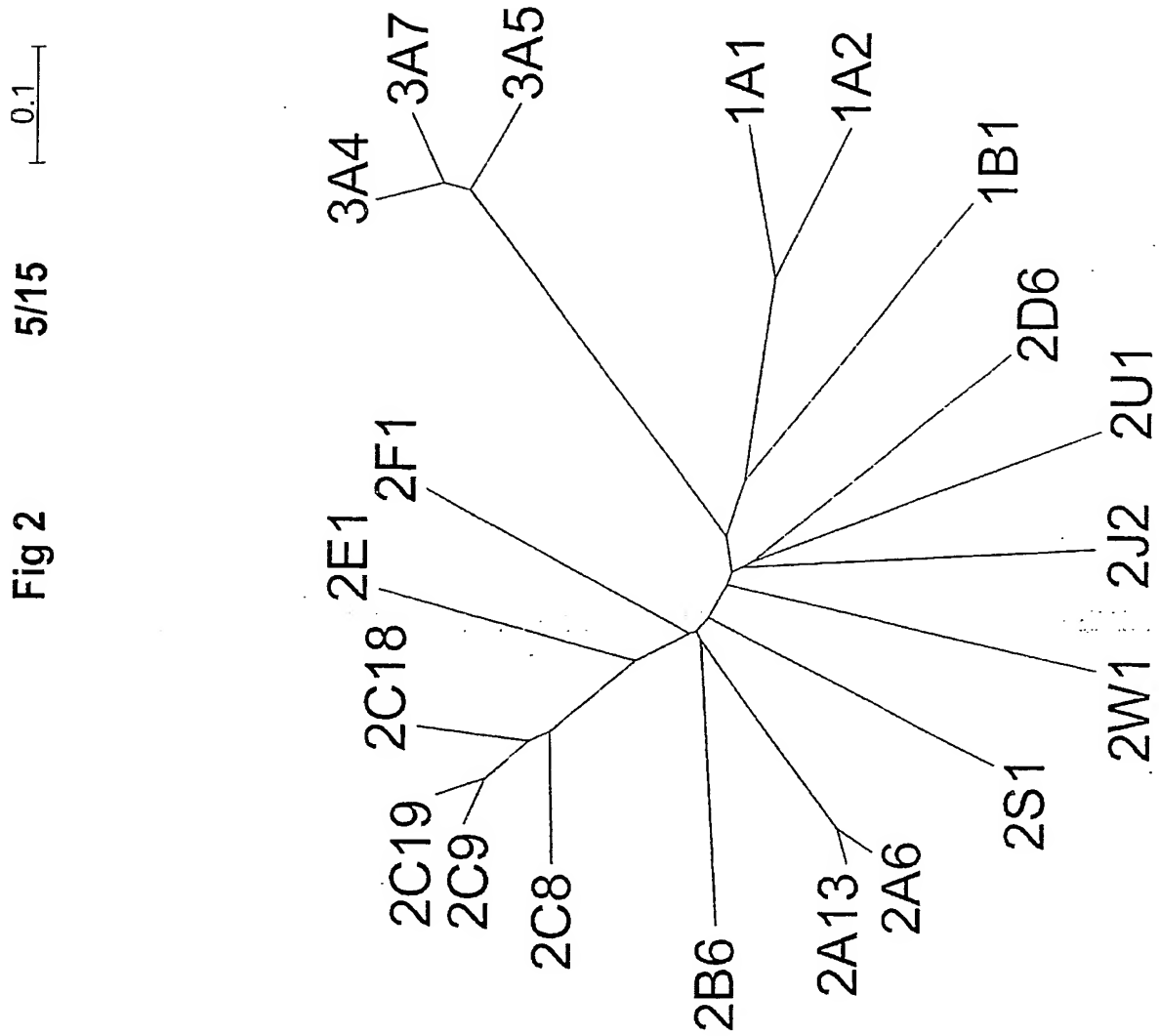
3/15

ttg ggg tcc cct ggc ctg cag ctg ttc aac gtc tac cca tgg ctc ggg Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly 210 215 220	672
gcc ctg ctc cag ctg cac cgg ccc gtc ctg cgc aag atc gag gag gtc Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val 225 230 235 240	720
cgt gcc att ctg agg acc ctc ctg gag gcg cgg agg ccc cac gtg tgc Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys 245 250 255	768
ccg ggg gac ccc gtg tgc agc tat gtg gac gcc ctg atc cag cag gga Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly 260 265 270	816
cag ggg gat gac ccc gag ggc ctg ttt gct gag gcc aac gcg gtg gcc Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala 275 280 285	864
tgc acc ctg gac atg gtc atg gcc ggg acg gag acg acc tcg gcc acg Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr 290 295 300	912
ctg cag tgg gcc gca ctt ctg atg ggc cgg cac ccg gac gtg cag ggc Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly 305 310 315 320	960
cgg gtg cag gag gag cta gac cgc gtg ctg ggc cct ggg cgg act ccc Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro 325 330 335	1008
cgg ctg gag gac cag cag gct ctg ccc tac aca agc gcc gtg ctc cac Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His 340 345 350	1056
gag gtg cag cgg ttc atc acg ctc ctg ccg cac gtg ccc cgc tgc acc Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr 355 360 365	1104
gcg gcc gac aca cag ctg ggc ggc ttc ctg ctc ccc aag ggc acg ccc Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro 370 375 380	1152
gtg att ccc ctg ctg acc tcg gtg ctc ctg gat gag aca cag tgg cag Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln 385 390 395 400	1200
acc cca ggc cag ttc aac ccc ggc cat ttc ctg gac gcg aat ggg cac Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His 405 410 415	1248

## Fig 1B (cont.)

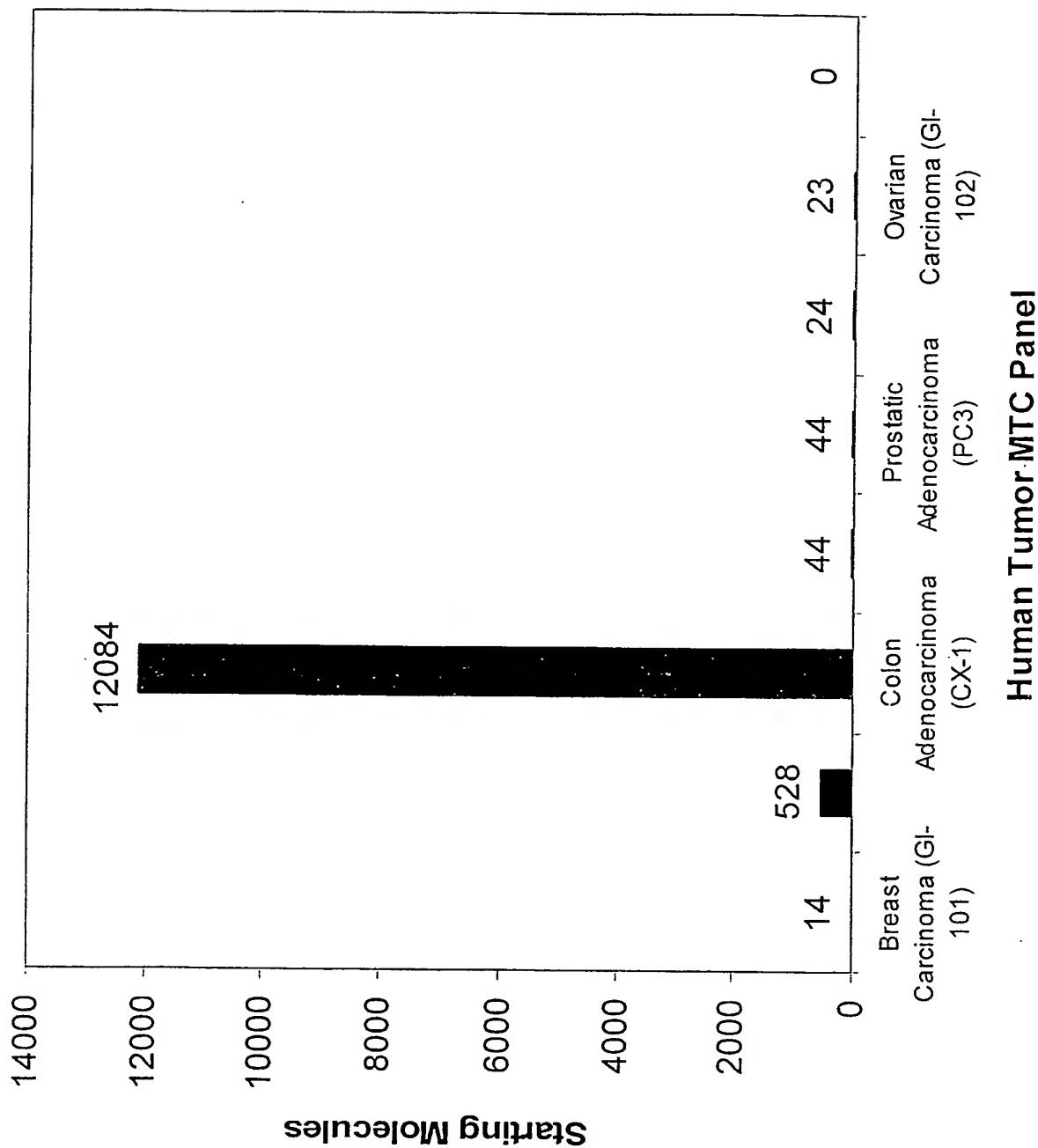
4/15

ttt gtg aag cgg gag gcc ttc ctg cct ttc tct gca ggc cgc cgc gtc	1296
Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val	
420 425 430	
tgt gtt ggg gag cgc ctg gcc agg acc gag ctc ttc ctg ctg ttt gcc	1344
Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala	
435 440 445	
ggc ctc ctg cag agg tac cgc ctg ctg ccc ccg cct ggc gtc agt ccg	1392
Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro	
450 455 460	
gcc tcc ctg gac acc acg ccc gcc cgg gct ttt acc atg agg ccg agg	1440
Ala Ser Leu Asp Thr Thr Pro Ala Arg Ala Phe Thr Met Arg Pro Arg	
465 470 475 480	
gcc cag gcc ctg tgt gcg gtg ccc agg ccc taggagctcc cccagccccc	1490
Ala Gln Ala Leu Cys Ala Val Pro Arg Pro	
485 490	
aggctctcct gaccactccc ctcccagccc tgggtctctcc caccctctct cctcccaccc	1550
cacagctcgg actgctctgg gagggccctg aggactccca ccctcacccc cccccaca	1610
gggtcagcaa ctgcttcgg ttacaccag gactaccct gcccgaccct gtgggacccc	1670
caccctctg atgotgtctg cagctcagtc cctgccagcc ccaggagcg cctccagggc	1730
cccgccact ctcccacccc tgaagctgca ctcccaccca cctagctccc cccaggggcc	1790
cccagcacct acagctgggg ctgcaggag acaacgggtg gctgcatcca gccagagaca	1850
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cacgaggtca ggagttcgag accagcctgc ccaacatggt gaaacctgt ctctactaaa	2270
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Fig 3 6/15



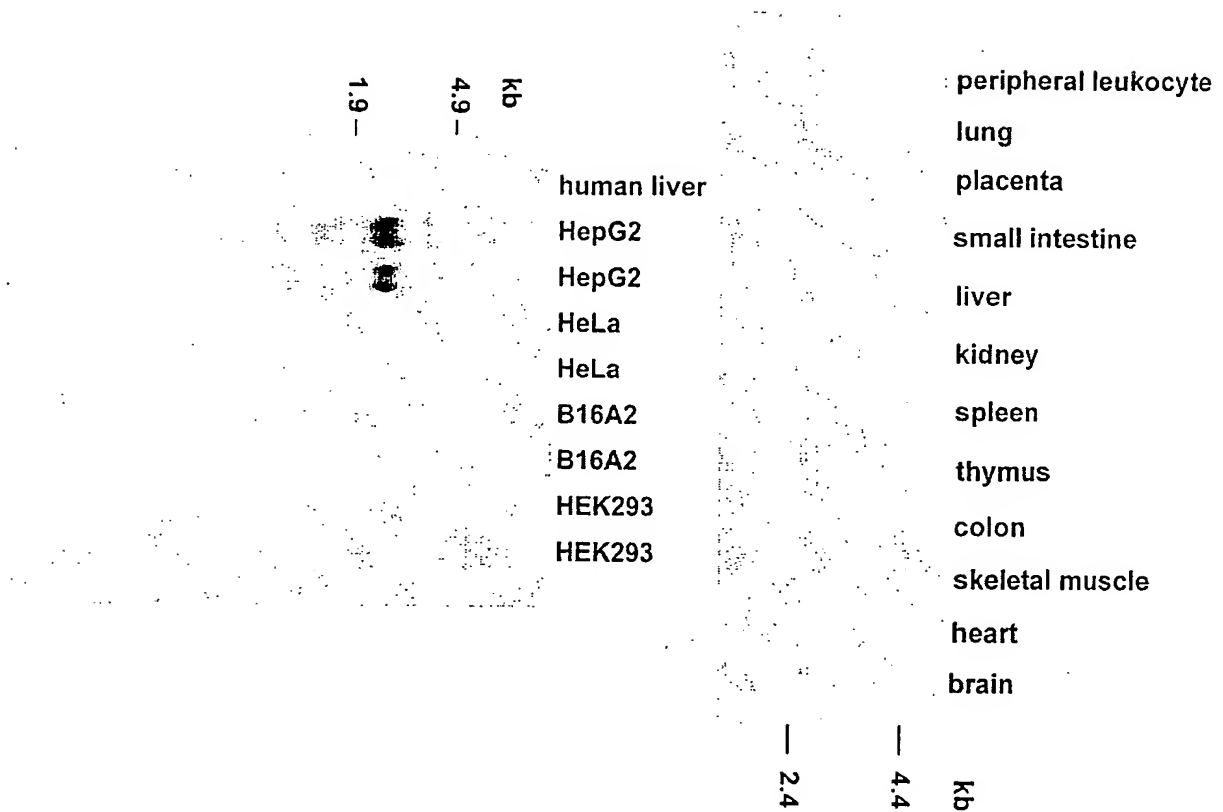
10/532014

Fig 4A 7/15

	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum left		heart	esophagus	colon transverse	kidney	lung	liver	leukemia HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum right	accumbens nucleus	aorta	stomach	colon descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia K-562	fetal kidney	<i>E. coli</i> rRNA
D	parietal lobe	amygdala		atrium right	jejunum		thymus	uterus	thyroid gland	leukemia MOLT-4	fetal liver	<i>E. coli</i> DNA
E	occipital lobe	caudate nucleus		ventricle left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma Raji	fetal spleen	Poly r(A)
F	temporal lobe	hippocampus		ventricle right	ileocecum		lymph node	testis		Burkitt's lymphoma Daudi	fetal thymus	human Cyt-1 DNA
G	paracentral gyrus of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma SW480	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon ascending		trachea			lung carcinoma A549		human DNA 500 ng

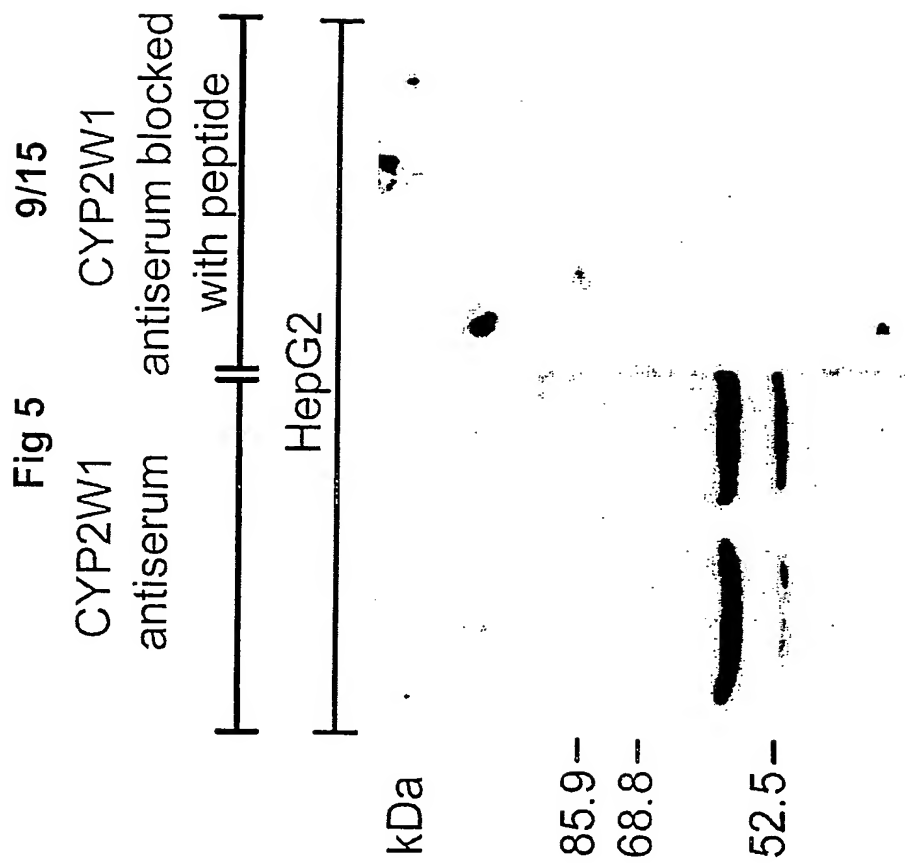
Fig 4B

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Fig 6 10/15

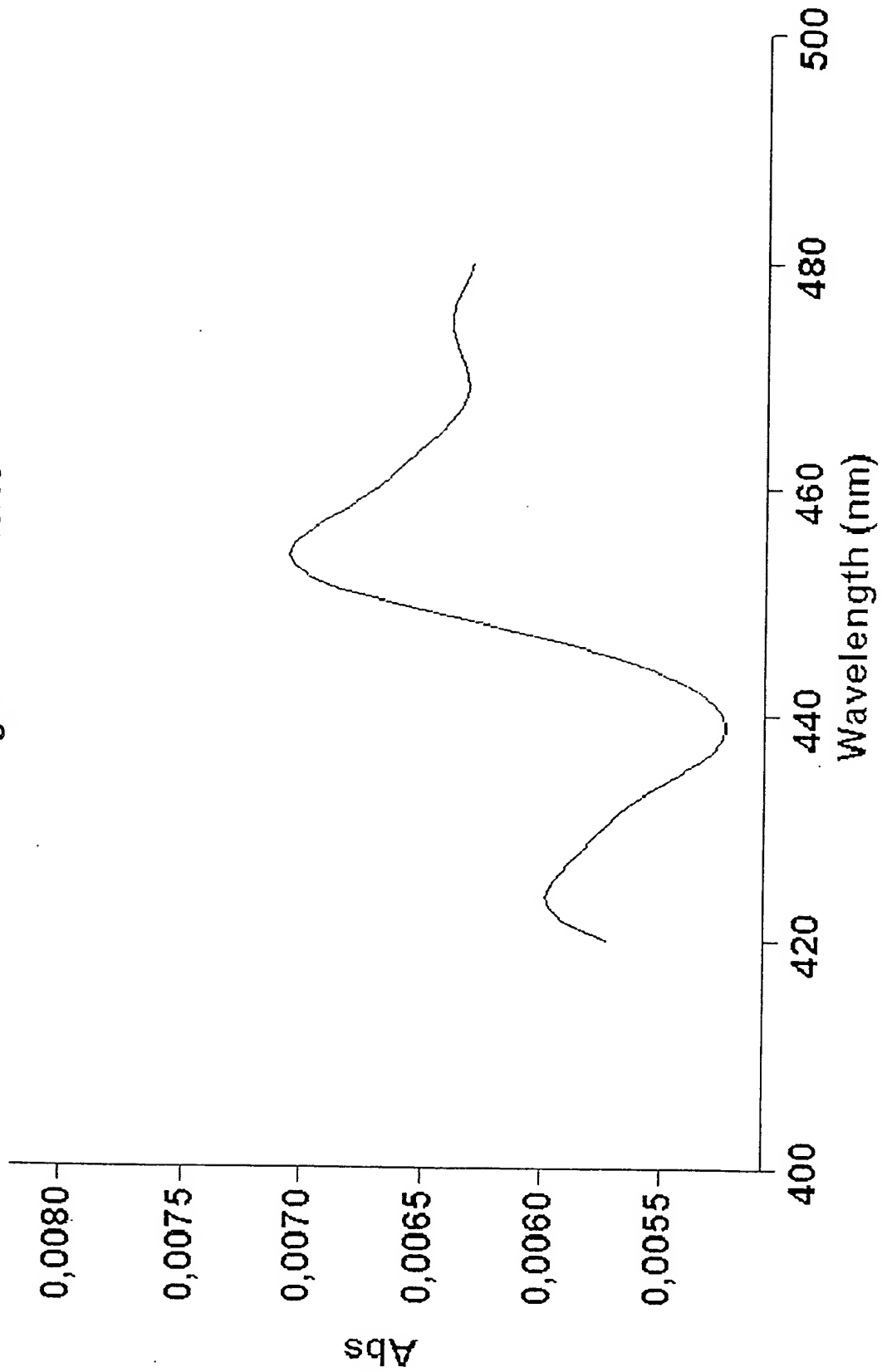


Fig 7 11/15

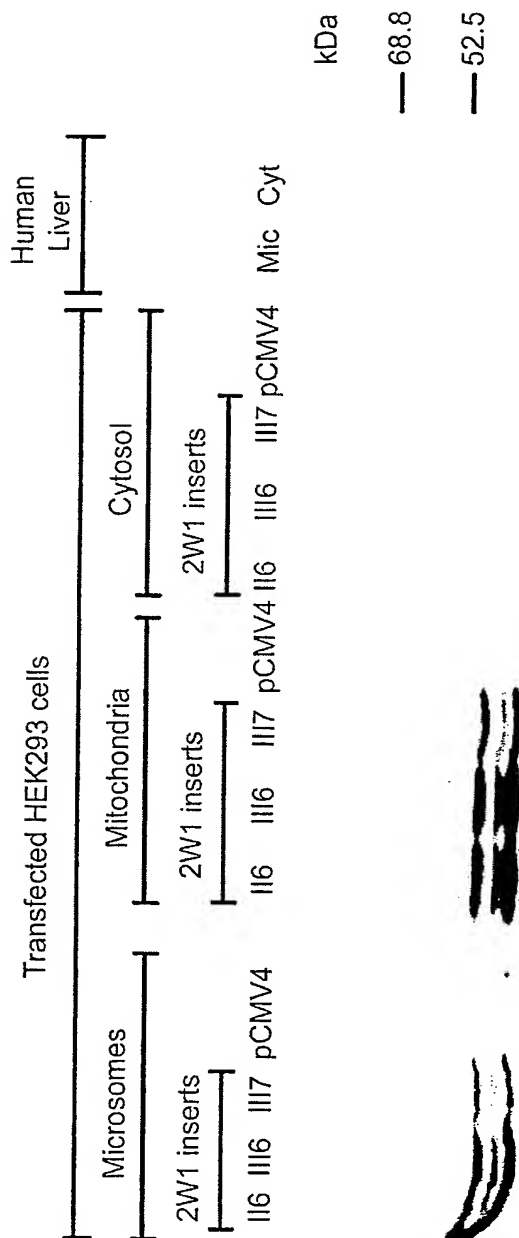


Fig 8 12/15

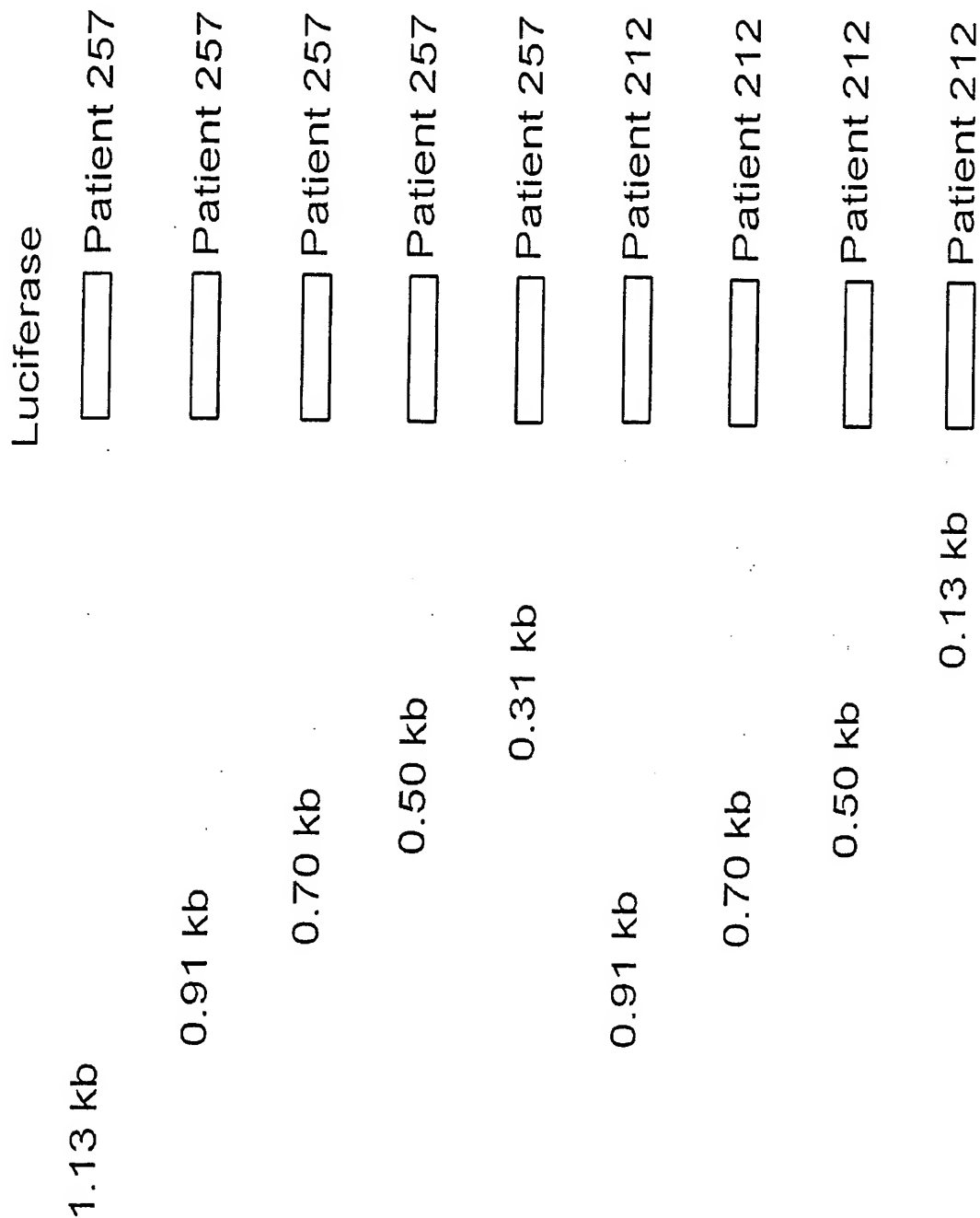


Fig 9 13/15

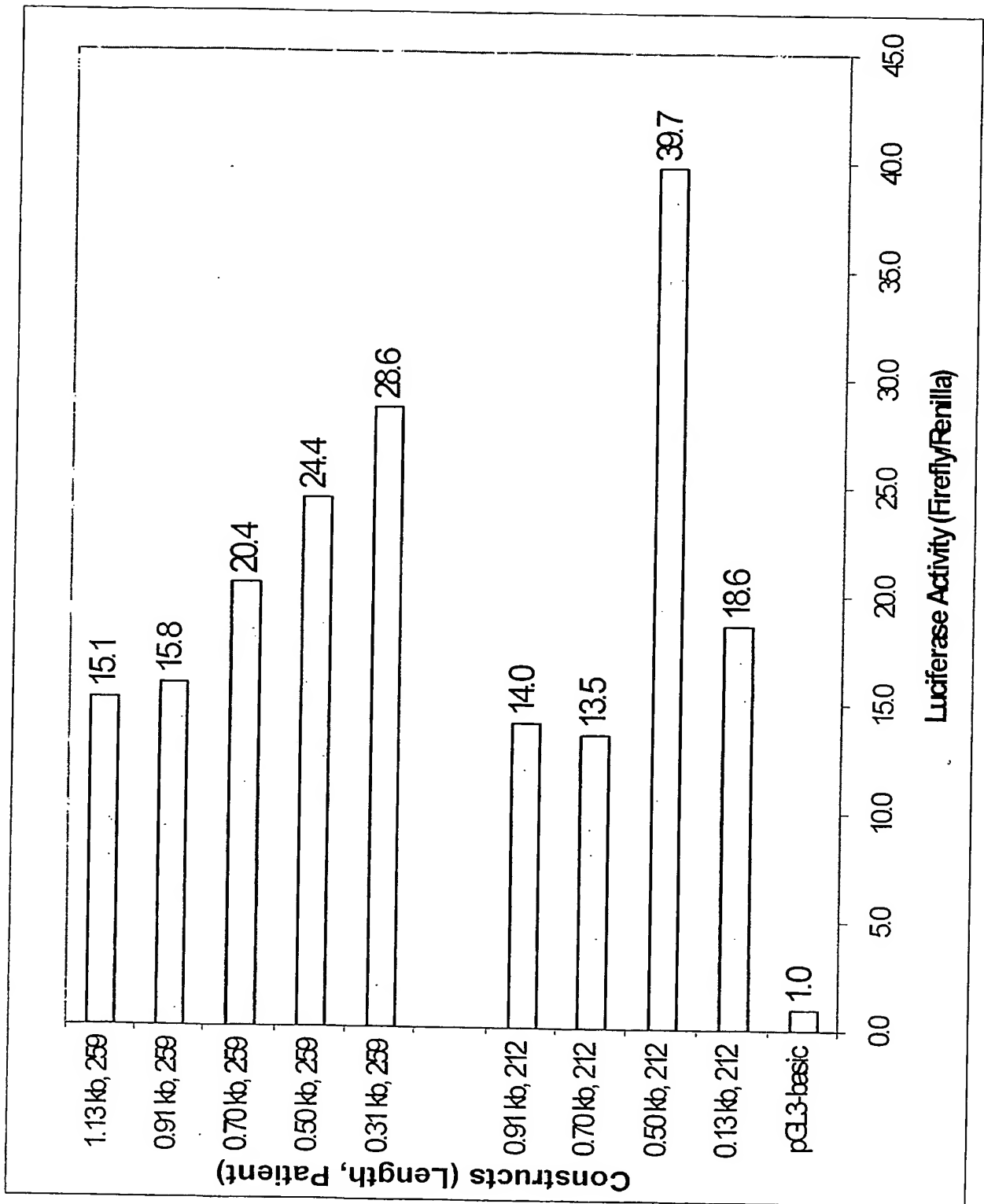


Fig 10 14/15

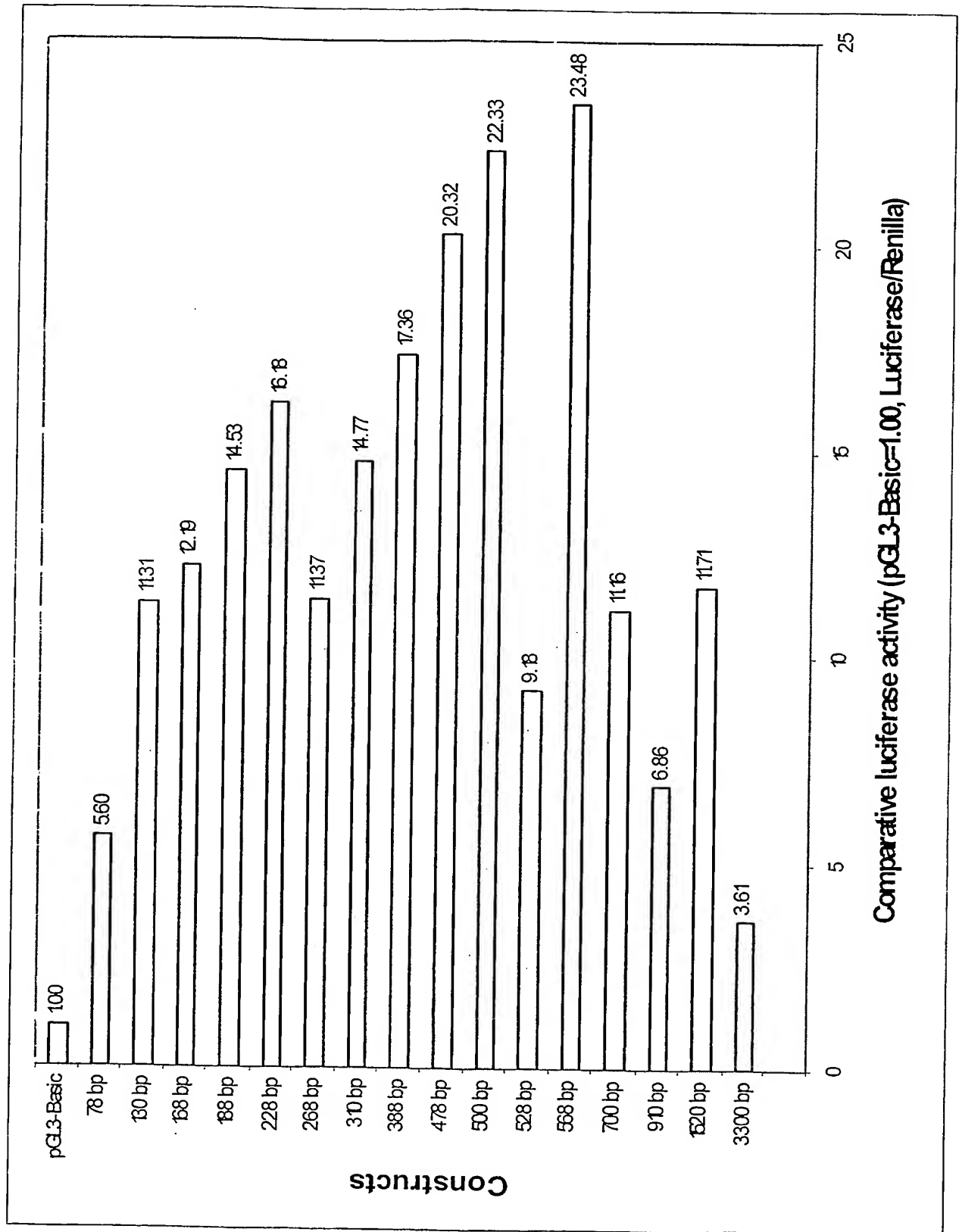
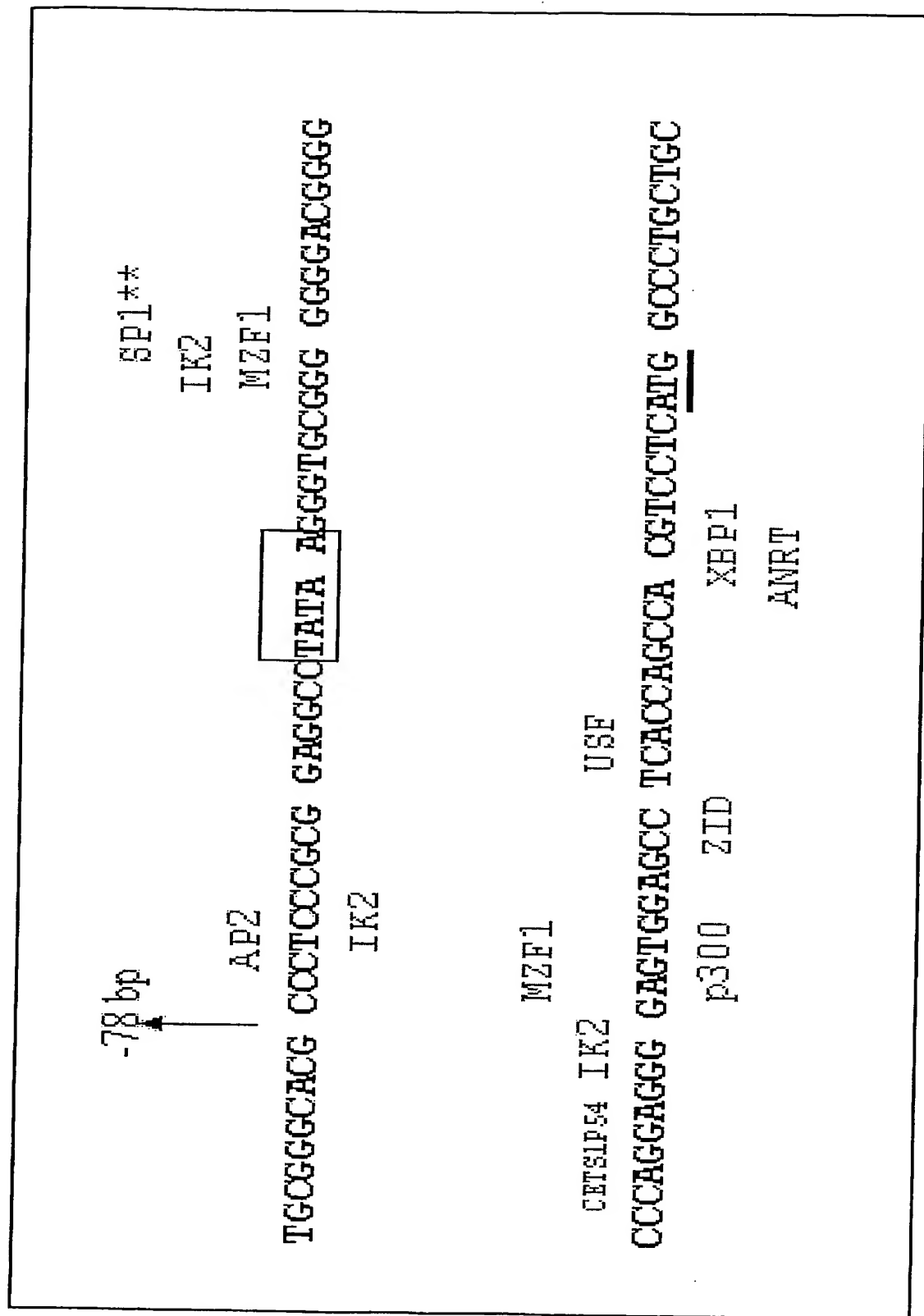


Fig 11 15/15



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